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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/091,442

DATE: 07/02/2002
TIME: 15:27:24

Input Set : N:\Crf3\RULE60\10091442.raw
Output Set: N:\CRF3\07022002\J091442.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:
 5 (i) APPLICANT: TSUJIMOTO, Masafumi
 6 IWASA, Fuyuki
 7 TSURUOKA, Nobuo
 8 NAKAZATO, Hiroshi
 9 MIURA, Kenju
 10 ISHIDA, Nobuhiro
 11 KURIHARA, Tatsuya
 12 YAMAICHI, Kozo
 13 YAMAGUCHI, Nozomi
 15 (ii) TITLE OF INVENTION: MEGAKARYOCYTE DIFFERENTIATION FACTOR
 17 (iii) NUMBER OF SEQUENCES: 34
 19 (iv) CORRESPONDENCE ADDRESS:
 20 (A) ADDRESSEE: Burns, Doane, Swecker & Mathis
 21 (B) STREET: P.O. Box 1404
 22 (C) CITY: Alexandria
 23 (D) STATE: Virginia
 24 (E) COUNTRY: United States
 25 (F) ZIP: 22313-1404
 27 (v) COMPUTER READABLE FORM:
 28 (A) MEDIUM TYPE: Floppy disk
 29 (B) COMPUTER: IBM PC compatible
 30 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 31 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
 33 (vi) CURRENT APPLICATION DATA:
 34 (A) APPLICATION NUMBER: US/10/091,442
 C--> 35 (B) FILING DATE: 07-Mar-2002
 C--> 36 (C) CLASSIFICATION:
 56 (vii) PRIOR APPLICATION DATA:
 41 (A) APPLICATION NUMBER: US/09/140,719
 42 (B) FILING DATE: 08-AUG-1998
 45 (A) APPLICATION NUMBER: US 08/474,661
 46 (B) FILING DATE: 07-JUN-1995
 49 (A) APPLICATION NUMBER: US 08/091,028
 50 (B) FILING DATE: 14-JUL-1993
 53 (A) APPLICATION NUMBER: JP 4-212305
 54 (B) FILING DATE: 17-JUL-1992
 57 (A) APPLICATION NUMBER: JP 6-067339
 58 (B) FILING DATE: 04-MAR-1993
 60 (viii) ATTORNEY/AGENT INFORMATION:
 61 (A) NAME: McGowan, Malcolm K.
 62 (B) REGISTRATION NUMBER: 39,300

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63 (C) REFERENCE/DOCKET NUMBER: 001560-247
65 (ix) TELECOMMUNICATION INFORMATION:
66 (A) TELEPHONE: (703) 836-6620
67 (B) TELEFAX: (703) 836-2021
70 (2) INFORMATION FOR SEQ ID NO: 1:
72 (i) SEQUENCE CHARACTERISTICS:
73 (A) LENGTH: 9 amino acids
74 (B) TYPE: amino acid
75 (C) STRANDEDNESS: single
76 (D) TOPOLOGY: linear
78 (ii) MOLECULE TYPE: peptide
80 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
82 Ser Glu Thr Ile Asn Cys His Phe Lys
83 1 5
86 (2) INFORMATION FOR SEQ ID NO: 2:
88 (i) SEQUENCE CHARACTERISTICS:
89 (A) LENGTH: 7 amino acids
90 (B) TYPE: amino acid
91 (C) STRANDEDNESS: single
92 (D) TOPOLOGY: linear
94 (ii) MOLECULE TYPE: peptide
96 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
98 Trp Gln Ser Ala Phe Thr Lys
99 1 5
102 (2) INFORMATION FOR SEQ ID NO: 3:
104 (i) SEQUENCE CHARACTERISTICS:
105 (A) LENGTH: 19 amino acids
106 (B) TYPE: amino acid
107 (C) STRANDEDNESS: single
108 (D) TOPOLOGY: linear
110 (ii) MOLECULE TYPE: peptide
112 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:
114 Val Glu Arg Val Asp Phe Thr Asn His Leu Glu Asp Thr Arg Arg Asn
115 1 5 10 15
117 Ile Asn Lys
121 (2) INFORMATION FOR SEQ ID NO: 4:
123 (i) SEQUENCE CHARACTERISTICS:
124 (A) LENGTH: 17 amino acids
125 (B) TYPE: amino acid
126 (C) STRANDEDNESS: single
127 (D) TOPOLOGY: linear
129 (ii) MOLECULE TYPE: peptide
131 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
133 Ser Tyr Ile Glu Val Thr Glu Glu Gly Thr Glu Ala Thr Ala Ala Thr
134 1 5 10 15
136 Gly
140 (2) INFORMATION FOR SEQ ID NO: 5:
142 (i) SEQUENCE CHARACTERISTICS:
143 (A) LENGTH: 9 amino acids

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144 (B) TYPE: amino acid
145 (C) STRANDEDNESS: single
146 (D) TOPOLOGY: linear
148 (ii) MOLECULE TYPE: peptide
150 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
152 Gln Tyr Leu Arg Ala Leu Gly Leu Lys
153 1 5
156 (2) INFORMATION FOR SEQ ID NO: 6:
158 (i) SEQUENCE CHARACTERISTICS:
159 (A) LENGTH: 20 amino acids
160 (B) TYPE: amino acid
161 (C) STRANDEDNESS: single
162 (D) TOPOLOGY: linear
164 (ii) MOLECULE TYPE: peptide
166 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:
168 Ala Asp Leu Ser Gly Ile Ala Ser Gly Gly Arg Leu Tyr Ile Ser Arg
169 1 5 10 15
171 Met Met Gly Lys
172 20
175 (2) INFORMATION FOR SEQ ID NO: 7:
177 (i) SEQUENCE CHARACTERISTICS:
178 (A) LENGTH: 5 amino acids
179 (B) TYPE: amino acid
180 (C) STRANDEDNESS: single
181 (D) TOPOLOGY: linear
183 (ii) MOLECULE TYPE: peptide
185 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:
187 Leu Tyr Asp Ala Lys
188 1 5
191 (2) INFORMATION FOR SEQ ID NO: 8:
193 (i) SEQUENCE CHARACTERISTICS:
194 (A) LENGTH: 5 amino acids
195 (B) TYPE: amino acid
196 (C) STRANDEDNESS: single
197 (D) TOPOLOGY: linear
199 (ii) MOLECULE TYPE: peptide
201 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:
203 Asn Tyr Glu Met Lys
204 1 5
207 (2) INFORMATION FOR SEQ ID NO: 9:
209 (i) SEQUENCE CHARACTERISTICS:
210 (A) LENGTH: 10 amino acids
211 (B) TYPE: amino acid
212 (C) STRANDEDNESS: single
213 (D) TOPOLOGY: linear
215 (ii) MOLECULE TYPE: peptide
217 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:
219 Ala Val Ala Met Met His Gln Glu Arg Lys
220 1 5 10

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223 (2) INFORMATION FOR SEQ ID NO: 10:
225 (i) SEQUENCE CHARACTERISTICS:
226 (A) LENGTH: 38 base pairs
227 (B) TYPE: nucleic acid
228 (C) STRANDEDNESS: single
229 (D) TOPOLOGY: linear
231 (ii) MOLECULE TYPE: DNA (genomic)
233 (ix) FEATURE:
234 (A) NAME/KEY: misc_feature
235 (B) LOCATION: 3..31
236 (D) OTHER INFORMATION: /note= "Corresponding to amino acid
237 sequence of SEQ ID NO: 3; N is inosine."
239 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:
241 GTNGARNNNNG TNGAYTYAC NAAYCAYYTN GARGAYAC 38
244 (2) INFORMATION FOR SEQ ID NO: 11:
246 (i) SEQUENCE CHARACTERISTICS:
247 (A) LENGTH: 32 base pairs
248 (B) TYPE: nucleic acid
249 (C) STRANDEDNESS: single
250 (D) TOPOLOGY: linear
252 (ii) MOLECULE TYPE: DNA (genomic)
254 (ix) FEATURE:
255 (A) NAME/KEY: misc_feature
256 (B) LOCATION: 9..28
257 (D) OTHER INFORMATION: /note= "Corresponding to amino acid
258 sequence of SEQ ID NO: 4; N is inosine."
260 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:
262 TACATCGANG TNACNGARGA RGGNACNGAR GC 32
264 (2) INFORMATION FOR SEQ ID NO: 12:
266 (i) SEQUENCE CHARACTERISTICS:
267 (A) LENGTH: 37 base pairs
268 (B) TYPE: nucleic acid
269 (C) STRANDEDNESS: single
270 (D) TOPOLOGY: linear
272 (ii) MOLECULE TYPE: DNA (genomic)
274 (ix) FEATURE:
275 (A) NAME/KEY: misc_feature
276 (B) LOCATION: 1..37
277 (D) OTHER INFORMATION: /note= "Oligomer attached to
278 3'-RACE kit (Gibco BRL)."
280 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:
282 GGCCACGCGT CGACTAGTAC TTTTTTTTTT TTTTTTTT 37
285 (2) INFORMATION FOR SEQ ID NO: 13:
287 (i) SEQUENCE CHARACTERISTICS:
288 (A) LENGTH: 20 base pairs
289 (B) TYPE: nucleic acid
290 (C) STRANDEDNESS: single
291 (D) TOPOLOGY: linear
293 (ii) MOLECULE TYPE: DNA (genomic)

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295 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:
 297 ATGTTGTGGG GACTGCTATA 20
 300 (2) INFORMATION FOR SEQ ID NO: 14:
 302 (i) SEQUENCE CHARACTERISTICS:
 303 (A) LENGTH: 23 base pairs
 304 (B) TYPE: nucleic acid
 305 (C) STRANDEDNESS: single
 306 (D) TOPOLOGY: linear
 308 (ii) MOLECULE TYPE: DNA (genomic)
 310 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:
 312 CAAGGCGAAT GACCTCTAAG TAT 23
 315 (2) INFORMATION FOR SEQ ID NO: 15:
 317 (i) SEQUENCE CHARACTERISTICS:
 318 (A) LENGTH: 21 base pairs
 319 (B) TYPE: nucleic acid
 320 (C) STRANDEDNESS: single
 321 (D) TOPOLOGY: linear
 323 (ii) MOLECULE TYPE: DNA (genomic)
 327 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:
 329 CCCCGAAGCA ATCCCAGAGA G 21
 332 (2) INFORMATION FOR SEQ ID NO: 16:
 334 (i) SEQUENCE CHARACTERISTICS:
 335 (A) LENGTH: 21 base pairs
 336 (B) TYPE: nucleic acid
 337 (C) STRANDEDNESS: single
 338 (D) TOPOLOGY: linear
 340 (ii) MOLECULE TYPE: DNA (genomic)
 342 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:
 344 CTCAGGCAGC AGAACGTACA T 21
 347 (2) INFORMATION FOR SEQ ID NO: 17:
 349 (i) SEQUENCE CHARACTERISTICS:
 350 (A) LENGTH: 21 base pairs
 351 (B) TYPE: nucleic acid
 352 (C) STRANDEDNESS: single
 353 (D) TOPOLOGY: linear
 355 (ii) MOLECULE TYPE: DNA (genomic)
 357 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:
 359 GCGCAGCAGCT CCTGGAGCCC G 21
 362 (2) INFORMATION FOR SEQ ID NO: 18:
 364 (i) SEQUENCE CHARACTERISTICS:
 365 (A) LENGTH: 22 base pairs
 366 (B) TYPE: nucleic acid
 367 (C) STRANDEDNESS: single
 368 (D) TOPOLOGY: linear
 370 (ii) MOLECULE TYPE: DNA (genomic)
 372 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:
 374 GACACCAGAC CAACTGGTAA TG 22
 377 (2) INFORMATION FOR SEQ ID NO: 19:
 379 (i) SEQUENCE CHARACTERISTICS:

VERIFICATION SUMMARY

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Input Set : N:\Crf3\RULE60\10091442.raw

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L:34 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:35 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:671 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:30